parental lines and heterozygous in the F_1 individual were identified. A sparse marker panel was developed as KASP for genotyping the F_2 lines for QTL mapping.

For nematode tolerance, one major QTL was detected on chrom 5 that explained 25% of the phenotypic variance. This QTL was further validated in an independent breeding panel of sugar beet breeding material. QTL mapping for cercospora resistance revealed a major QTL on chromosome 4 detected in three of the four locations tested and explaining up to 30% of the genetic variance.

DNA of F2 individuals at the extreme of the phenotypic distribution for the traits under consideration is currently combined into pools and sequenced with Illumina technology. Allele frequencies for variants will be determined for both pools. Deviations in allele frequencies between the pools should identify the genomic loci responsible for the quantitative traits. In order to pinpoint to the causal genes, the candidate regions will then be further analyzed with regard to e.g. functional gene annotation and the impact of variant positions in the diverse alleles.

W1018: Sugar Cane (ICSB)

Leveraging Multiple Sequencing Technologies to Generate a Haplotype Specific Assembly of Sugarcane R570

Adam Healey[1], John Lovell[2], Olivier Garsmeur[3], Jerry Jenkins[2], Jane Grimwood[2], Karen Aitken[4], Robert J. Henry[5], Angélique D'Hont[3], Jeremy Schmutz[2] and HudsonAlpha-Genome Sequencing Center, (1)HudsonAlpha Institute For Biotechnology, Huntsville, AL, (2)HudsonAlpha Institute for Biotechnology, Huntsville, AL, (3)CIRAD, UMR AGAP, Montpellier, France, (4)CSIRO Agriculture and Food, St Lucia, Australia, (5)University of Queensland/QAAFI, Brisbane, QLD, Australia

While sugarcane is one of the world's most important economic grasses for its sugar production and biofuel potential, tools and resources to understand its genetics are lacking. This is owed to the complexity of its genome which is highly polyploid, aneuploidy and heterozygous. Additionally, modern sugarcane cultivars are the result of interspecific hybridization and repeated backcrossing between domesticated *S. officinarium* and wild *S. spontaneum* parents. Cultivar R570 is best characterized sugarcane genome to date with the release of the BAC clone single tiling path, but this assembly represents a gene-rich and collapsed view of each of R570's homeologous chromosomes. To generate a haplotype specific assembly of R570, we devised a strategy that combines two *de novo* assemblies of R570 (Illumina; Pacbio), 96 selfed offspring (15X cov), single chromosome libraries and HiC to sequence and separate each homeologous chromosome. Using Illumina libraries, we generated a 5 Gb *de novo* genome assembly, using it to extract 55 Million unique 80bp genetic markers. Genotyping these markers in 96 selfed offspring isolated 1.9 million simplex (single dose) markers that were projected onto the 7.4 Gb PacBio assembly to generate a genetic map and anchor contigs onto separate linkage groups. Contigs that cannot be anchored by simplex markers will be ordered and oriented using HiC contact maps and single chromosome libraries. This strategy of combining multiple sequencing technologies will generate a more complete assembly for one of the most complex genomes to date in the Plant Kingdom.

W1019: Sugar Cane (ICSB)

Sequencing the Transcriptome of R570 to Explore the Complexity of the Sugarcane Genome

Adhini Sudhindra Kumar Pazhany[1], Virginie Perlo[2], Frikkie Botha[3], Agnelo Furtado[3], Angela O'Keeffe[4], Ardy Kharabian Masouleh[4], Robert Henry[5], Karen Aitken[6], Angelique d'Hont[7], Adam Healey[8], Jane Grimwood[9], Kerrie Barry[10] and Jeremy Schmutz[9], (1)Queensland Alliance for Agriculture and Food Innovation,The University of Queensland, St Lucia, QLD, Australia, (2)University of Queensland, Brisbane, Australia, (3)University of Queensland/QAAFI, Brisbane, QLD, Australia, (4)QAAFI (Queensland Alliance for Agriculture and Food Innovation), The University of Queensland, Brisbane, QLD, Australia, (5)Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD, Australia, (6)CSIRO Agriculture and Food, St Lucia, Australia,